

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using SW model.
Run on: September 4, 2002, 13:53:36 ; Search time 165.17 Seconds

(without alignments)
315.394 Million cell updates/sec

Title: US-09-052-089a-1.
Perfect score: 2384
Sequence: 1 MPIRALCITCSDFFDHSRDV.....VRVKTVPSLFQAKLDTFLWS 469
Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5
Searched: 74754 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 74754
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:*

3: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

4: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

5: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:*

6: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1986.DAT:*

7: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1987.DAT:*

8: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1988.DAT:*

9: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1989.DAT:*

10: /SIDS5/gcdata/geneseq/geneseq/geneseq-emb1/AA1990.DAT:*

11: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1991.DAT:*

12: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1992.DAT:*

13: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1993.DAT:*

14: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1994.DAT:*

15: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1995.DAT:*

16: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1996.DAT:*

17: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1997.DAT:*

18: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1998.DAT:*

19: /SIDS5/gcdata/geneseq/geneseq-emb1/AA1999.DAT:*

20: /SIDS5/gcdata/geneseq/geneseq-emb1/AA2000.DAT:*

21: /SIDS5/gcdata/geneseq/geneseq-emb1/AA2001.DAT:*

22: /SIDS5/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

| | | | | | | |
|----|-------|-----|------|----|----------|---------------------------------------|
| 12 | 170.5 | 7.2 | 1456 | 22 | ABBS8673 | Drosophila melanogaster |
| 13 | 170 | 7.1 | 951 | 22 | ABBS9033 | Drosophila melanogaster |
| 14 | 169.5 | 7.1 | 484 | 22 | ABM78985 | Human protein SEQ |
| 15 | 169 | 7.1 | 1690 | 22 | ABB61144 | Drosophila melanogaster |
| 16 | 169 | 7.1 | 1690 | 22 | ABB61173 | Drosophila melanogaster |
| 17 | 168 | 7.0 | 1325 | 20 | ABW19540 | Male-enhanced anti-mouse male enhance |
| 18 | 168 | 7.0 | 934 | 22 | AAW94391 | Human secreted pro-domestic mite Bt1 |
| 19 | 167.5 | 7.0 | 1017 | 22 | AAE02466 | Human phosphodiesterase |
| 20 | 167.5 | 7.0 | 2517 | 21 | AAV71159 | Drosophila melanogaster |
| 21 | 167.5 | 7.0 | 482 | 22 | ABE71396 | Drosophila melanogaster |
| 22 | 167 | 7.0 | 2067 | 22 | ABE7125 | Domestic mite Bt1 |
| 23 | 167 | 7.0 | 875 | 22 | ABE0245 | Domestic mite Bt1 |
| 24 | 166.5 | 7.0 | 808 | 22 | ABE02242 | Domestic mite Bt1 |
| 25 | 166.5 | 7.0 | 1177 | 22 | ABW6721 | Human protein SEQ |
| 26 | 166 | 7.0 | 1960 | 22 | ABM7854 | Novel human diagno |
| 27 | 166 | 7.0 | 2143 | 22 | ABG01716 | Novel human diagno |
| 28 | 165.5 | 6.9 | 2954 | 20 | AAV01632 | Streptococcus pyogenes |
| 29 | 164.5 | 6.9 | 690 | 22 | ABM80122 | Novel protein SEQ |
| 30 | 164.5 | 6.9 | 880 | 22 | ABR96332 | Putative P. abyssi |
| 31 | 164 | 6.9 | 808 | 22 | ABG05140 | Novel human diagno |
| 32 | 164 | 6.9 | 2442 | 21 | ARY77575 | Putative P. abyssi |
| 33 | 164 | 6.9 | 441 | 10 | ABW90955 | Human cytoskeletal |
| 34 | 163.5 | 6.9 | 441 | 14 | ABR47780 | M6 streptococcal p |
| 35 | 163.5 | 6.9 | 441 | 14 | ABR47780 | Human polypeptide |
| 36 | 163.5 | 6.9 | 483 | 18 | ABW0927 | Type 6 M-protein |
| 37 | 163.5 | 6.9 | 1213 | 22 | ABM40016 | Human polypeptide |
| 38 | 163.5 | 6.9 | 1639 | 22 | ABR59807 | Drosophila melanogaster |
| 39 | 163.5 | 6.9 | 1752 | 20 | ARY0031 | Breast cancer asso |
| 40 | 163.5 | 6.9 | 1988 | 22 | ABM40099 | Human polypeptide |
| 41 | 163.5 | 6.9 | 1988 | 22 | ABM41000 | Drosophila melanogaster |
| 42 | 163.5 | 6.9 | 2779 | 22 | ABE62371 | Novel human diagno |
| 43 | 163.5 | 6.9 | 2918 | 22 | ABG77218 | Novel human diagno |
| 44 | 163 | 6.8 | 721 | 21 | ABE21227 | Novel human diagno |
| 45 | 163 | 6.8 | 1717 | 22 | ABG20672 | Novel human diagno |

ALIGNMENTS

RESULT 1
ID AAY30149 standard; Protein: 469 AA.

AC AAY30149;

XX 27-OCT-1999 (first entry)

DT Amino acid sequence of a BRCA1 modulator protein.

DE Modulator protein; BRCA1; tumour suppressor protein; breast cancer;

KW ovarian cancer; cell growth; cell proliferation.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 3..32
FT /note= "zinc finger motif"
FT 230..255
FT /note= "leucine zipper motif"
FT XX

PN US5948643-A. .

XX PD 07-SEP-1999.

XX PF 13-AUG-1997; 97US-0968751.

XX PR 13-AUG-1997; 97US-0968751.

XX DR WPI; 1999-517952/43.

Human male enhance

| | | | |
|---------------------|--|---|-----|
| Db | 241 | selfqaklelkssqkdlassadkeimslkkklmlgetinlpvasetvdrvlvespape | 300 |
| QY | 301 | VNLKLRSPFRDDIDLNATFDVTPPARSSQHGGYERKLEKSHSPIDVPKICKGP | 360 |
| Db | 301 | vnkllrrpsfrddidlnatfdvtpparssqhggyeklekhspidvpkickgp | 360 |
| QY | 361 | RKSQLSGGQSCAGEPDEELVGAFPIVRNAILQKQPKRPRSESSSKDWRTGFDL | 420 |
| Db | 361 | rksqls1gqscagepdeelvgafpivrnailqkqpkprsescskdavrtgfqgl | 420 |
| QY | 421 | GGRTKFTQPTDMIRPLVKPKTKVKQRVRVKTWPSLRFQAKLDTFLMS | 469 |
| Db | 421 | GGRTKFTQPTDMIRPLVKPKTKVKQRVRVKTWPSLRFQAKLDTFLMS | 469 |
| QY | 187 | MVGQSAVEQAVYCVSLKEVENLK---EARKSGEVADKLKDLSR | 233 |
| Db | 187 | MVGQSAVEQAVYCVSLKEVENLK---EARKSGEVADKLKDLSR | 233 |
| QY | 234 | -----SKLQTYSELD-----OAKL---ELKSAQKLOSA---DKEIMSLKK | 270 |
| Db | 234 | -----SKLQTYSELD-----OAKL---ELKSAQKLOSA---DKEIMSLKK | 270 |
| Db | 239 | fidmcsfdcskleervshlesdlyqaqeklqafenktaylsdspascqqlsnialkre | 298 |
| QY | 271 | LTMQETINLNPVVASETVDRVLVLESPARPEVNLKLRSPFRDDIDLNATFDVTPPARPS | 330 |
| Db | 271 | LTMQETINLNPVVASETVDRVLVLESPARPEVNLKLRSPFRDDIDLNATFDVTPPARPS | 330 |
| QY | 331 | SSQHGYE-----KICLEKSH-SPTOVPKICKGPKRPRSESSSKDWRTG---FDGLGRTK | 425 |
| Db | 331 | SSQHGYE-----KICLEKSH-SPTOVPKICKGPKRPRSESSSKDWRTG---FDGLGRTK | 425 |
| QY | 380 | ELVGAFPIFVRNAILQKQPKRPRSESSSKDWRTG---FDGLGRTK | 425 |
| Db | 380 | ELVGAFPIFVRNAILQKQPKRPRSESSSKDWRTG---FDGLGRTK | 425 |
| QY | 327 | sssvgiahlnktngniglakskipkgvg-----ggvsmstgtrktss | 371 |
| Db | 327 | sssvgiahlnktngniglakskipkgvg-----ggvsmstgtrktss | 371 |
| XX | 372 | dlskysif-----kkprllgssssaltattqsnfvngmogsek | 413 |
| PN | W0200171042-A2. | | |
| XX | 27-SEP-2001. | | |
| PD | 23-MAR-2001; 2001WO-US09231. | | |
| PF | XX | | |
| PR | 23-MAR-2000; 2000US191637P. | | |
| PR | 11-JUL-2000; 2000US0-0614150. | | |
| PA | XX | | |
| (PEKE) PE CORP NY. | | | |
| XX | | | |
| PA | (PEKE) PE CORP NY. | | |
| XX | | | |
| PI | Venter JC, Adams M, Li PWD, Myers EW; | | |
| XX | | | |
| DR | WPI; 2001-658660/75. | | |
| XX | | | |
| DR | N-PSDB; ABL05392. | | |
| XX | | | |
| PT | New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - | | |
| XX | | | |
| PS | Disclosure; SEQ ID NO 10659; 21pp + Sequence Listing; English. | | |
| XX | | | |
| CC | The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB011676, AB030511), expressed DNA sequences (AB01840-ABL16175) and the encoded proteins (ABL0777-ABL07207). | | |
| CC | The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences . | | |
| SQ | Sequence 455 AA; | | |
| PA | | | |
| XX | | | |
| PS | W020153312-A1. | | |
| XX | | | |
| PD | 26-JUL-2001. | | |
| XX | | | |
| PF | 26-DEC-2000; 2000WO-US34263. | | |
| XX | | | |
| PR | 21-JAN-2000; 2000US-0488725. | | |
| PR | 25-APR-2000; 2000US-0552317. | | |
| PR | 09-JUL-2000; 2000US-0598042. | | |
| PR | 19-JUL-2000; 2000US-0620312. | | |
| PR | 03-AUG-2000; 2000US-0653450. | | |
| PR | 14-SEP-2000; 2000US-0662191. | | |
| PR | 19-OCT-2000; 2000US-0693035. | | |
| PR | 29-NOV-2000; 2000US-0727344. | | |
| XX | | | |
| PA | (HYSE-) HYSEQ INC. | | |
| XX | | | |
| PI | Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; | | |
| PI | Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J; | | |
| PI | Zhao QA, Zhou P, Goodrich R, Drmanac RT; | | |
| XX | | | |
| DR | WPI; 2001-442253/47. | | |
| DR | N-PSDB; AAI58253. | | |

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries
 XX
 PS Example 4; SEQ ID NO 2242; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI5798-AAI61369) and
 CC the encoded polypeptides (AM38642-AM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 2663 AA:
 SQ
 Query Match 7.9%; Score 187.5; DB 22; Length 2663;
 Best Local Similarity 25.1%; Pred. No. 7.9e-06;
 Matches 93; Conservative 66; Mismatches 133; Indels 79; Gaps 18;
 QY 55 KRPIINKLFEDLAQEEENVLDRFLKNEQDNLNRAQLSQDKDE-RDSQVDTLRTLEE 113
 Db 1632 kmtnavn-----etgkmcielehkqefetqklnlenieneritqj---lhenlee 1680
 QY 114 RKAIVVLSLQQLGKAEMCSTUKKQMKYLEQODET---KQAEQEG---RLRSKMT 165
 Db 1681 mr-svtkerddirsve---etikverdqklenlretitrldiekqeeikivhmlkehqet 1736
 QY 166 MEOIELLQSQLEPEVEEMIRDMGVGOSAV-----EOLAVYCVSKKEYENLKEARKA 217
 Db 1737 idklrigiveksteisnqdklehsndalkaqdklqiqeketidkrgi 1796
 QY 218 SGIVADKL--RKDLFSSRSKQTVVSDAKLELSAQDKLQOSADK--EIMSIKK- 270
 Db 1797 vsektdklsnqdklensnakiqekigekelkanehqlttkkownetqkvsmeqikkqi 1856
 QY 271 -----TMLQ-ETLNLPPVASEETVDRU-----VLEPAPPVENLKURRPSRERDI--- 314
 Db 1857 kdslitiskleinenltaqelheneleemksvnkardhrvvetklerdaklesiqetk 1916
 QY 315 -DLNATPFDVDPMPARSSSSQH---GYYEKLC-----LEKSHSPIQDVPKK 355
 Db 1917 ardeleiqeket--armiskehketvdakirekisektiqisdiqkdkskdelq--kk 1971
 QY 356 ICKGPRESQ 366
 Db 1972 iqelqkkelql 1982
 RESULT 5
 ID AAM40883 standard; Protein; 2688 AA.
 AC AAM40883;
 XX DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 5814.
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 PS WO200133312-A1.
 XX
 PR 25-APR-2000; 200005-0552317.
 PR 09-JUL-2000; 200005-0598042.
 PR 19-JUL-2000; 200005-0520312.
 PR 03-AUG-2000; 200005-053450.
 PR 14-SEP-2000; 200005-0662191.
 PR 14-OCT-2000; 200005-0593036.
 PR 29-NOV-2000; 200005-0727344.
 PR
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehnman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RR;
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI60039.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries.
 XX Example 2; SEQ ID NO 5814; 10078pp; English.
 CC The invention relates to human nucleic acids (AAI5798-AAI61369) and
 CC the encoded polypeptides (AM38642-AM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 2688 AA:
 SQ
 Query Match 7.9%; Score 187.5; DB 22; Length 2688;
 Best Local Similarity 25.1%; Pred. No. 7.9e-06;
 Matches 93; Conservative 66; Mismatches 133; Indels 79; Gaps 18;
 QY 55 KRPIINKLFEDLAQEEENVLDRFLKNEQDNLNRAQLSQDKDE-RDSQVDTLRTLEE 113
 Db 1656 kmtnavn-----etgkmcielehkqefetqklnlenieneritqj---lhenlee 1704
 QY 114 RKAIVVLSLQQLGKAEMCSTUKKQMKYLEQODET---KQAEQEG---RLRSKMT 165
 Db 1705 mr-svtkerddirsve---etikverdqklenlretitrldiekqeeikivhmlkehqet 1760
 QY 166 MEOIELLQSQLEPEVEEMIRDMGVGOSAV-----EOLAVYCVSKKEYENLKEARKA 217
 Db 1761 idklrigiveksteisnqdklehsndalkaqdklqiqeketidkrgi 1820
 QY 218 SGIVADKL--RKDLFSSRSKQTVVSDAKLELSAQDKLQOSADK--EIMSIKK- 270
 Db 1821 vsektdklsnqdklensnakiqekigekelkanehqlttkkownetqkvsmeqikkqi 1880

XX Human TRAP coding sequences, used to treat transport disorders and
 PT cancer
 XX
 PS Claim 1; Page 74-77; 87pp; English.
 XX
 CC This sequence represents human transport-associated protein-8 (TRAP-8).
 CC The DNA sequence was first identified in a human colon tissue
 CC cDNA library. The full-length cDNA was derived from a series of
 CC overlapping and/or extended cDNA sequences and is a consensus.
 CC TRAP-8 to 9 (AAV31639-Y31647) are a novel group of proteins with
 CC chemical and structural homology that are involved in molecular
 CC transport. Various disorders are associated with defects in the transport
 CC of molecules, either intracellularly or to the extracellular
 CC environment. Examples of such disorders include cystic fibrosis,
 CC multidrug resistance, hypercholesterolaemia and certain forms of diabetes
 CC mellitus. Defective nuclear transport may play a role in cancer. For
 CC example, the BRCA1 protein, associated with familial breast cancer, is
 CC normally imported into the nucleus via nuclear pore complexes, but is
 CC aberrantly located in the cytoplasm in breast cancer cells. In other
 CC cancers, cells can secrete excessive amounts of hormones e.g. cancers of
 CC the adrenal medulla can secrete excessive amounts of adrenaline and
 CC noradrenaline, leading to hypertension. TRAP is expressed in cancer
 CC cells, and transport disorders result from either excessive or
 CC insufficient molecular transport. Anti-TRAP antibodies and nucleic acids
 CC encoding TRAP can be used as diagnostic tools for such disorders. TRAP
 CC antagonists can be used to treat or prevent a cancer associated with
 CC increased TRAP expression. Anti-TRAP antibodies can be used directly
 CC as an antagonist or as a targeting mechanism for drugs. Alternatively,
 CC a TRAP antisense nucleotide can be used to treat cancers. A TRAP
 CC agonist or expression vector may be used to treat a disorder caused by
 CC reduced transport of biologically active molecules.
 XX Sequence 962 AA;

Query Match 7.5%; Score 178; DB 20; Length 962;
 Best Local Similarity 20.4%; Pred. No. 1.1e-05; DB 20; Length 962;
 Matches 76; Conservative 62; Mismatches 92; Indels 142; Gaps 11;

QY 52 QVGKRITINKLEF-----DLAQEEENVLDBREFLK-NELDNV-RAQLS 91
 DB ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

AC AAM79969;
 XX DT 06-NOV-2001 (first entry)

XX DE Human Protein SEQ ID NO 3615.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.
 XX PN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PR 05-FEB-2001; 2001WO-US04098.

XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-0560875.

XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.

XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 15-SEP-2000; 2000US-0663561.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.

XX PA (HYSE-) HYSEQ INC.
 XX DR WPI; 2001-476283/51.
 XX DR NPDB; AAK53102.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -

XX PS Claim 20; Page 397; 6221pp; English.

CC The invention relates to polynucleotides (AAK5145-AAK5435) and the
 CC encoded polypeptides (AAK8323-AAM8020) that exhibit activity relating to
 CC cytokine or cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The polynucleotides and
 CC polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC antiinflammatory activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM8020) are omitted as the relevant pages from the sequence listing
 XX were missing at the time of publication.
 XX Sequence 533 AA;

Query Match 7.3%; Score 174.5; DB 22; Length 533;
 Best Local Similarity 20.2%; Pred. No. 9.7e-06; Matches 86; Conservative 84; Mismatches 155; Indels 101; Gaps 15;

QY 30 HQCLQISFEAPSRICPQCRIQVG-----KRTIN---KLFFDLAQE----- 70
 DB 15 hievkes1-takegraailqtevdairlreeketmlnkktkq1gdmeeakgtqagein 73

QY 71 -ENVLPRE-----FLKNEFLDVRQAOLSQDKREKRSQVDTLRTLEERNATVSLQ 123
 DB 74 dkdmldvkerkvnlgkienlqeqldkekqmslkirkvsklgdttntdtaitltee 133

QY 124 ALGKAEMLCSSTLKKQMLQEQQDTEKQQAQEBAGRRLSKMKTMEQIETLQLSQLPEVEEM 183

RESULT 9
 ID AAM79969
 ID AAM79969 standard; Protein: 533 AA.
 XX

| | |
|-----------|---|
| PS | Claim 1; Page 12-15; 21pp; Japanese. |
| CC | The present sequence represents the human male enhanced antigen-2 (MER-2). The present invention also described an antibody specific for the MEA-2 protein. The antibody can be used for the identification of a gene causing diseases related to spermatogenesis. The MET-2 nucleotide sequence is useful as a chromosome marker, and in the detection of pancreatic cancer. |
| CC | The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences . |
| CC | Disclosure; SEQ ID NO 2811; 21pp + Sequence Listing; English. |
| XX | Best Local Similarity 7.2%; Score 172.5; DB 22; Length 1374; Matches 72; Conservative 57; Mismatches 120; Indels 43; Gaps 9; |
| QY | 35 I0SFETAPSRTPQCRIQVGKRTIINKLFFDLAQEEENVLREFLKEYD----IVRA 88 Db 1084 ikrelenskkialelehekgkgtgiggssnaa-rehnnsal-rehnnsal-talakreadiylvqnlvqa 1142 |
| QY | 89 QLSQKDKEKRDQSOVQIDTLDLEERNATVWSQOALGKAEMLCSTLKKQMLEQQDE 148 Db 1143 vlrqkeeedrqmkhvlqgqalslekekeksvnslikeqyaaavkveaghnrhfkastlse 1202 |
| QY | 149 TK-----QAEQEAQRLRSKMKTME---QIEL-----LQSOLPEVEEM 183 Db 1203 vkkhelgakehvlrqklgqeadlqiegkhsqeqaqaaeaaqrqqlqkql--deg 1259 |
| QY | 184 IRDGMGVQASAVRQLAVCVSLLKEYENLKEARAKASGVAKDRLDLSRSKLTQVSEL 243 Db 1260 lskqpvqngememlkwvedqkereiqsikqqlaltdeqg--rkelqglqllqnvksel 1316 |
| QY | 244 DQAKLELKSAQKDLQSADEKIMSLKKL-TMEOET---LNUPPVASETVD 290 Db 1317 emaqedlsmtqkdkfmlqkvselknmkmtllqngqkldirrgaaktvrl 1368 |
| RESULT 12 | |
| ABB58673 | ABB58673 standard; Protein; 1456 AA. |
| XX | AC ABB58673; |
| DT | 26-MAR-2002 (first entry) |
| XX | Drosophila melanogaster polypeptide SEQ ID NO 2811. |
| KW | Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. |
| OS | Drosophila melanogaster. |
| PN | WO200171042-A2. |
| PD | 27-SEP-2001. |
| PF | 23-MAR-2001; 2001WO-US09231. |
| PR | 23-MAR-2000; 2000US-191637P. |
| PR | 11-JUL-2000; 2000US-0614150. |
| XX | (PKEE) PE CORP NY. |
| PA | |
| XX | ABB59033 standard; Protein; 951 AA. |
| PT | Venter JC, Adams M, Li PWD, Myers EW; |
| XX | WPI: 2001-656860/75. |
| DR | N-PSDB; ABL02776. |
| PT | New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - |
| XX | |
| SQ | Sequence 1374 AA; |
| PS | Best Local Similarity 20.1%; Score 170.5; DB 22; Length 1456; Matches 116; Conservative 97; Mismatches 202; Indels 163; Gaps 222 |
| QY | 15 DHSDRVAIIH--CGHPTHLQCLIQSFTAPSRTCPOCRIQVGKRTIINKLFFDLQEEE 71 Db 55 dyqrhavikescikaceehymnlgtdrem----farleeknriketktgl---q 104 |
| QY | 72 NVLDRERFLKNELDNVRAQLQSQDKKEKRDQSOVQIDTLDLEERN----- 115 Db 105 tvqernritseiteldhmdikdrkisvlqrkienledlikdnqvdmarsangah 164 |
| QY | 116 -----ATVSLQOALGKAEMLCSTLKKQMKYEQQQETKQ-----AQEE 155 Db 165 hssegaltsleaaqgdkekqmaqlqdrdahenkqdhervadykiklraese 224 |
| QY | 156 AGRLSKMK---TMEOETL---QSL---PEVEMIRDMGVGSAVEOLAVCVSL 204 Db 225 veklqtrleravtererleikiesaqsglkskakelatcengrassadwestqkriarl 284 |
| QY | 205 KKEYENLKEARAKS-----GEVADKLRKDFSSRSKLTQVYSELDQA 246 Db 285 elenerikhdersqftfgrttmttsqeldraegeradkasaellrqaelrvtsqdaera 344 |
| QY | 247 KLLIKSACKDQLQSADEKIMSLKKLTMU---OPTLNUP-PVASETVDRLVLESPPAVEVN 302 Db 345 reaaaalqeklsqeqyvrlkaklenqagqeqsrlqeqekasgqsrhadrdrasev 404 |
| QY | 303 LKURRPSFRDDIDLNAIFDVDTTPARFSSQHGYEKI---CLEKHSPI---QDVPRKIC 357 Db 405 ek-keemertqalg-----ksqlqh---eklqnsidkagnedvhldqkldkac 450 |
| QY | 358 KGPRK-----EQSLSG-GOSCKAGEPDBELVGAFFPVRNAT----LG 395 Db 451 tennrlvlekek1tydylqlsqdkalqgaarmqkaretisldtkirekletqvqlg 510 |
| QY | 396 OKPDKR-----PRSESCS-----KDVRTRGFGIGLGRKFQOPTDPMIR 436 Db 511 rikeerdkfsdeletkperseasqtlmkaadreanmqdlevker----- 557 |
| QY | 437 PLPVPKPKVKQVRVK----TVPFLQAKLDTFLW 469 Db 558 --yekshaiqqlqmerddayteveilkekdkalya 592 |
| RESULT 13 | |
| ABB59033 | ABB59033 standard; Protein; 951 AA. |
| XX | AC ABB59033; |
| XX | 26-MAR-2002 (first entry) |
| XX | Drosophila melanogaster polypeptide SEQ ID NO 3891. |
| KW | Drosophila; developmental biology; cell signalling; insecticide; |

| | |
|-----------------------|---|
| KW | pharmaceutical. |
| XX | |
| OS | Drosophila melanogaster. |
| XX | |
| PN | WO200171042-A2. |
| XX | |
| PD | 27-SEP-2001. |
| XX | |
| PF | 23-MAR-2001; 2001WO-US09231. |
| XX | |
| PR | 23-MAR-2000; 2000US-191637P. |
| XX | |
| PR | 11-JUL-2000; 2000US-0014150. |
| XX | |
| XX | (PEKE) PE CORP NY. |
| PA | |
| XX | Venter JC, Adams M, Li PW, Myers EW; |
| PI | |
| XX | WPI; 2001-656860/75. |
| DR | N-PSDB; ABL03136. |
| XX | |
| PT | New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions . |
| PR | |
| XX | PS Disclosure; SEQ ID NO 3891; 21pp + Sequence Listing; English. |
| XX | |
| CC | The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABJ6176 ABJ3051), expressed DNA sequences (ABJ0840 ABJ16175) and the encoded proteins (ABB7737-ABB72072). |
| CC | The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences . |
| CC | |
| SQ | Sequence 951 AA: |
| Query Match | 7.1%; Score 170; DB 22; Length 951; |
| Best Local Similarity | 20.9%; Pred. No. 5e-05; |
| Matches | 94; Conservative 91; Mismatches 157; Indels 108; Gaps 19; |
| Qy | 72 NYLDR-EFLKNELDNVRAQLSQLDKRDSQVYID-----TLRDTLEERNATVSQLGLG 126 |
| Db | 333 npldrghkqklyralgnkkrkeerrlkleernqelvldndnqsvql-ethl 391 |
| Qy | 127 KAEMLCSTLKKOMKYLROQDDETKQAOEEAGRLSKUMTMEQIELLKLQSQLPEVEEMIRD 186 |
| Db | 392 egkm---rlenkvkamagelleepqkhrssqesvhqsinsivaerdairekrqgie--- 444 |
| Qy | 187 MGVGQSAVEQLAVWCYSLKEVNLKARK--ASGEVADKLK-----KDLFSSR 234 |
| Db | 445 -----dleglkqkngnslqrnydqsgnqeqnrgirtrrtdnlrlehrkkllrdsgreve 498 |
| Qy | 235 KIQTWVSELDQAKLLEMSKQDQSAD--KETMSLKKITMLOETLNPPVASETVPRLV 292 |
| Db | 499 rkklysdiaatkdesqyeirklesdtkeldqgranolatqrgnlaemkseelkll 558 |
| Qy | 293 LESPAPVENVK-LRPSFRD-----DIDLNATFDV 322 |
| Db | 559 eteklsheridqairqrserereavavakessencskciesiaeitkaeqliqlqn 618 |
| Qy | 323 DTPPARP-SSQHGYEKLCLBKSHSPIDQPKKICKGPRKRSQLSUGGQSCAGEPDEEL 381 |
| Db | 619 nsmqakelkeleh-----aleqsknlgaeqkeliensnkgdelis-----diker 663 |
| Qy | 382 VGFPIFVRRNATLGQKOPKKRPSSESSCSKDVVRTGFGLGGKFTQPTDTVMIRPLVK 441 |
| Db | 664 akqfeayir-----qgeehkqknktp-----spksnsyspsd----pspk 700 |
| RESULT | 14 |
| Qy | 442 PKTK---VKQRFRVKTPSLFOAKLDPF 466 |
| Db | 701 eltnqirirlieqvr-demaklfaaelkrf 729 |
| XX | |
| XX | AAM78985 |
| ID | AAM78985; Standard; Protein; 484 AA. |
| XX | |
| AC | AAM78985; |
| XX | |
| DT | 06-NOV-2001 (first entry) |
| XX | |
| DE | Human protein SEQ ID NO 1647. |
| XX | |
| KW | Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulator; cancer; leukaemia; nervous system disorder; arthritis; inflammation. |
| KW | |
| OS | Homo sapiens. |
| XX | |
| PN | WO20015190-A2. |
| XX | |
| PD | 09-AUG-2001. |
| XX | |
| PF | 05-FEB-2001; 2001WO-US04098. |
| XX | |
| PR | 03-FEB-2000; 2000US-0496914. |
| XX | |
| PR | 27-APR-2000; 2000US-0560875. |
| XX | |
| PR | 20-TUN-2000; 2000US-0598075. |
| XX | |
| PR | 19-JUL-2000; 2000US-0620325. |
| XX | |
| PR | 15-SEP-2000; 2000US-0644936. |
| XX | |
| PR | 20-OCT-2000; 2000US-0693325. |
| XX | |
| PR | 30-NOV-2000; 2000US-0728422. |
| XX | |
| PA | (HYSE-) HYSEQ INC. |
| XX | |
| PI | Tang YT, Liu C, Drimanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y; |
| PI | Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; |
| PI | Xue AJ, Yang Y, Weijhrman T, Goodrich R; |
| XX | |
| DR | WPI; 2001-476283/51. |
| XX | |
| N-PSDB | AAK52118. |
| XX | |
| PT | Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy . |
| XX | |
| PS | Claim 20; Page 3984-3985; 6221pp; English. |
| XX | |
| CC | The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AMW83208030) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. |
| CC | Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AMW802020) are omitted as the relevant pages from the sequence listing were missing at the time of publication. |
| CC | |
| XX | |
| SQ | Sequence 484 AA: |
| Query Match | 7.1%; Score 169.5; DB 22; Length 484; |
| Best Local Similarity | 20.3%; Pred. No. 2.2e-05; |
| Matches | 75; Conservative 72; Mismatches 143; Indels 79; Gaps 11; |

genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -
 PT
 PT
 Disclosure; SEQ ID NO 10311; 21pp + Sequence Listing; English.
 XX
 CC
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL6176-ABL30511), expressed DNA sequences (ABL0180-ABL1515) and the encoded proteins (ABR57737-ABR72072).
 CC
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1690 AA;

Query Match 7.1%; Score 169; DB 22; Length 1690;
 Best Local Similarity 20.7%; Pred. No. 0.00014; Indels 76; Gaps 13;
 Matches 83; Conservative 84; Mismatches 158;

QY 50 RIVGKRTINKLFFDIAQEEENVNLDRFLKNE--LDRVAGDLSOKKEKRSQVDTL 107
 Db 724 qdilekesieqqi--alknqleldfqkkqkqseseevhleikagntqkdfelvsgesikk 781

QY 108 RDLLEERNATVLSQQLGKAEMLCSTLKKQW-YLHQDQDTIQQEEAGRLSKRMK 166
 Db 782 qgqleqktlgkhklaal-----eekkeketikekeqglqqiqksaasesalkvv 834

QY 167 E-QIELLQSQLEPEVEENIRDGMVGOSAVEQIAYVCVSLKKEYE----- 209
 Db 835 qvqleqiqqgaaasgegegsktralhseisqkqsetqsklqsnleakskqleaa 894

QY 210 -NUKEARKASGEVAD--KLRSDFSSRKQTVYBQLDQAKLLELSAQDLSADKEI 264
 Db 895 ngsleeeakksghllegitklskevgetqaalsschdvesktkqleaanaalekvnky 954

QY 265 MSLKKKLUMLQEMTNLNPPVASEEDVDRIVLESAPPVEV--LKKRSDFRDDI----DLN 317
 Db 955 aesaeraasdldqkv-----keitdtihaelgaersssalhtklsfsdeatgkhelt 1008

QY 318 ATFDV-----DTPPARSSQHGYEYKLEKSHSPIDQVPRKIC 357
 Db 1009 skdawawsqmlqkekkelqelrqqlqdsgsqkkaegerkeksfees---iknlgveet 1065

QY 358 KGPKESQSLGQSCAGEPDESLVGFAPPFRNALIGOKO 398
 Db 1066 kattenlelstgttikldqerle-----itnaelghke 1100

RESULT 17
 AAW19540
 ID AAW19540 standard; Protein; 1325 AA.
 XX
 AC AAW19540;
 XX
 DT 16-SEP-1997 (first entry)
 DE Male-enhanced antigen-2.
 XX
 KW Mouse; MEA-2; detecting mutation.
 XX
 OS Mus musculus domesticus.
 XX
 FH Key Location/qualifiers
 FT Misc-difference 305..320
 FT /note= "Not shown in the specification"
 XX
 PN JP09121869-A.
 XX

PD 13-MAY-1997.
 XX
 PF 07-NOV-1995; 95JP-0311638.
 XX
 PR 07-NOV-1995; 95JP-0311638.
 XX
 PA (ITOH-) ITO HAM KK.
 XX
 DR WPI: 1997-314229/29.
 DR N-PSSB; RATT4034.
 XX
 PT Male-enhanced antigen Mea-2
 PS detecting mutation(s)
 XX
 CC The present sequence represents male-enhanced antigen-2 (MEA-2), which has been derived from a domestic mouse. The polynucleotide encoding the protein can be used for the detection of mutations affecting the MEA-2 gene.
 XX
 SQ Sequence 1325 AA;

Query Match 7.0%; Score 168; DB 18; Length 1325;
 Best Local Similarity 20.6%; Pred. No. 0.00012; Indels 102; Gaps 13;
 Matches 77; Conservative 65; Mismatches 130;

QY 68 QEEENVLDREFLKNELD----NVRQLSQKDEKRSQVDTLDRTEERNATVSL 121
 Db 966 rehnsiletalakreadlqvlnlqvgavqlqrkeedrqmqlvqajqvslekekmen 1025

QY 122 QQAIGKA-----EMCSTLKKQMYLEQO---QDER 149
 Db 1026 keqmaarieaghnrhrfkaatlelsevkelqakehlgvtiqaevedelqdgkhsqe 1085

QY 150 KQAEQEEGRRSRKMTKQDQILOLLOSLQPEVEEMIRDGMVGOSAVDOLAVCVSLKKEYE 209
 Db 1086 aqfqtelaeartqqlq-----l1qkkl---deqmsqgqptgsgemdkweldqkerei 1135

QY 210 NUKEARKASGEVADKLKDFSSRSRKQTVYBQLDQAKLLELSAQDLSADKEIMLK 269
 Db 1136 slkqqlqldteqg----kkelqdtqqtqgtissemewqedisetqkdfmlqakvselkn 1192

QY 270 KI-TMLOBT-----LNIP--PVASETVDRLVLESPA 297
 Db 1193 mntklqgqnlqkldirrgaakkkepkgesqsspatpiklpcprpasleellirppa 1252

QY 298 ---PVEVNKLRRPSFRDDI-LNATFDPVDPAPRSPSSQHGYYKLCLKSHSPIDV 352
 Db 1253 vskepl-nlnaclqqkqemolslqrqmehitvhessswaqveaapahah---- 1305

QY 353 PRKICKGPRKESQL 366
 Db 1306 -----prgdtkl 1312

RESULT 18
 AAW94391
 ID AAW94391 standard; Protein; 1325 AA!
 XX
 AC AAW94391;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE Mouse male enhanced antigen 2.
 XX
 KW Mouse; male enhanced antigen 2; Mea-2; Mus musculus domesticus;
 KW Spermatogenesis; regulation; contraceptive; sterile; inhibition.
 OS Mus sp.
 XX
 PN JP11018622-A.

| | |
|-----------------------|--|
| XX | WO200027861-A1.. |
| PN | |
| PR | 12-NOV-1999; 9900-US26860. |
| XX | 12-NOV-1998; 9800-0108255. |
| PD | 18-MAY-2000. |
| XX | |
| PF | (SIRRD) UNIV LELAND STANFORD JUNIOR. |
| XX | |
| PI | Conti M., Pahlke G. |
| XX | |
| DR | WPI; 2000-316479/32. |
| DR | N-PSDB; AAD00769. |
| XX | |
| PT | Polynucleotide encoding a phosphodiesterase (PDE) interacting protein, useful for diagnosis and treatment of asthma, cystic fibrosis, Crohn's disease, and rheumatoid arthritis - Disclosure; Fig 5; 77pp; English. |
| XX | |
| PS | The present sequence is a phosphodiesterase (PDE) interacting protein, myomegulin obtained from two human clones KIAA0454 and KIAA0477. The myomegulin gene is located on human chromosome 1P35.1-p36. The protein modulates the functions and properties of PDEs, specifically cAMP-PDEs, and also targets them to specific subcellular compartments. The present sequence can be used in the diagnosis and treatment of disease conditions associated with PDE activity. The diseases include asthma, cystic fibrosis, inflammatory airway disease, chronic bronchitis, eosinophilic granuloma, psoriasis, proliferative skin diseases, endotoxic shock, septic shock, ulcerative colitis, Crohn's disease, reperfusion injury, inflammatory arthritis, atopic dermatitis, urticaria, adult respiratory distress syndrome, diabetes insipidus, allergic rhinitis, allergic conjunctivitis, vernal conjunctivitis, arterial restenosis, atherosclerosis, inflammatory diseases associated with irritation and pain, rheumatoid arthritis, ankylosing spondylitis, transplant rejection and graft versus host disease, disease conditions associated with hypersecretion of gastric acid, and disease conditions in which cytokines are mediators. |
| XX | |
| SQ | Sequence 2517 AA; |
| Query Match | 7.0%; Score 167.5; DB 21; Length 2517; |
| Best Local Similarity | 22.8%; Pred. No. 0.00031; Mismatches 91; Conservative 82; Mismatches 139; Indels 87; Gaps 21; |
| Matches | 91; Conservative 82; Mismatches 139; Indels 87; Gaps 21; |
| Qy | 24 HCGHTF-HQCLQTSFETAPSRTCPQCRCRQVGRKTINKLFLDAQEEENVLREF-LKN 81 |
| Db | 601 hlnhslshkeqlqef-----reliqyrdnsdklteamnl-lekirkrihdavaler 653 |
| Qy | 82 ELDNVRQAQSQKDEKEKRDQSVII-----DTLRTDLERFERNATVLSQOALG---KAEM 130 |
| Db | 654 aidekfksaleekelrqlrlavrverdhlerikdvlssneatingmsmellrakgleveq 713 |
| Qy | 131 LCSTLKKQKYLEQODERK---QAQEDAGRURSKMKTMEQIELLQLQPEVEE--- 182 |
| Db | 714 l-sstccqnlqlwkleem-ektfksrwqkeggs-----1liqqqtslhinkeredst 763 |
| Qy | 183 MIRDGMVGGSQAV-FOLAVCVSLKKEVENUEKARAKASGEVADKLKDINSSRK----- 235 |
| Db | 764 lickgpgseiaeel--cqrlqrk-----ermlqdlisdrnkqylehe 805 |
| Qy | 235 -----LQTVYSELQDAKELLSAQKDLQSADEKTMSSLKLTQIOTELNLPPASETWD 289 |
| Db | 805 meiqqlqlqgqvstreqesqqaeklvgqnlmernsseqnlqylggdsinsqapinsqng 865 |
| Qy | 290 -----RLVESPAPVEVNKLRRPSFRDDIDLNATFDVWNPAPPSSQHGGYYKLC-LE 343 |
| Db | 866 vtpqgrlqkqdqg----smqisprddstslakedvsip----ristgldtvagle 915 |
| XX | |
| SQ | Sequence 482 AA; |
| Query Match | 7.0%; Score 167; DB 22; Length 482; |
| Best Local Similarity | 20.8%; Pred. No. 3.4e-05; Mismatches 74; Conservative 59; Mismatches 101; Indels 122; Gaps 14; Matches 74; Conservative 59; Mismatches 101; Indels 122; Gaps 14; |
| Db | 175 cpyclermdevsdgvtitlcnhafhasclmkwgds-----tcpvcvhwqtbgvlvedsvcmc 230 |
| Qy | 7 CTICSOFPDHSDR-WAIIHGHTFHQCLQTSFETAPSRTCPQCRCRQVGRKTINKLFLDAQEEENVLREF-LKN 50 |
| Db | 51 -----IQGVGRKTINKLFLDAQEEENVLREF-LKN 72 |
| Db | 231 cegtslwiclicqgvcgryggahaahfratnntfamqlgtsav-----wdya-gdn 283 |
| Qy | 73 VLDREFLKLNDUNVRAQLSOKDKEKRDQSVIQTDLERFERNATVLSQOALGAEMLC 132 |
| Db | 284 fvhrlf-qnksdg-kivasqtekdereeki----dsmq-----mefytlit 323 |

| | | | | | |
|-----------------------|--|---|---------|------------|------|
| QY | 133 | SPILKKQKMKYLEQQDETAKQACEE---AGRLRSKMKTMEQIELLOLQSOLQPEVEEMIRDW | 188 | | |
| Db | 324 | sqldtqkyeeyermerlieqewqnhkatandaktevselqiqqgnmkqekvnlealdhankanaeaqknkyqqqlkdqtaledqeqradda | 376 | | |
| QY | 189 | VGOSAVELAVVCKSLKREYENKEARKASGEVADKLRRDFSSRSRKLQTVSELDOAKL | 248 | | |
| Db | 377 | -----rklqhtakiklkdqkqlneer-----elskalqsnqsswhgkylleqyn | 422 | | |
| Oy | 249 | ELKSAQKDLQSADKEIMSLKKKLTML-----QETLNLPVPASETVDRVLVLESPAP | 298 | | |
| Db | 423 | efk-----qthdaevtelkedlrdimflndnqklaanteiaggtvgtgiaekedp | 472 | | |
| RESULT | 23 | | | | |
| ID | ABB71125 | ABB71125 standard; Protein: 2067 AA. | | | |
| XX | | | | | |
| AC | ABB71125; | | | | |
| XX | | | | | |
| DT | 26-MAR-2002 | (first entry) | | | |
| XX | | | | | |
| DE | Drosophila melanogaster | polypeptide SEQ ID NO 40167. | | | |
| XX | | | | | |
| KW | Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. | | | | |
| XX | | | | | |
| OS | Drosophila melanogaster. | | | | |
| XX | | | | | |
| PN | WO200171042-A2. | | | | |
| XX | | | | | |
| PD | 27-SEP-2001. | | | | |
| XX | | | | | |
| PF | 23-MAR-2001; | 2001WO-US09231. | | | |
| XX | | | | | |
| PR | 23-MAR-2000; | 2000US-191637P. | | | |
| PR | 11-JUL-2000; | 2000US-0614150. | | | |
| XX | | | | | |
| PA | (PEKE) | PE CORP NY. | | | |
| XX | | | | | |
| PI | Venter JC, | Adams M, | Li PWD, | Myers EW; | |
| XX | | | | | |
| DR | WPI; | 2001-656860/75. | | | |
| DR | N-PSDB; | ABLI5228. | | | |
| XX | | | | | |
| PS | New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - Disclosure: SEQ ID NO 40167; 21pp + Sequence Listing; English. | | | | |
| PT | The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABLI3051), expressed DNA sequences (ABLI0840-ABLI175) and the encoded proteins (ABBL7737-ABBL2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. | | | | |
| XX | Sequence | 2067 AA; | | | |
| SQ | | | | | |
| Query Match | 7.0% | Score 167; DB 22; Length 2067; | | | |
| Best Local Similarity | 20.5% | Score 167; DB 22; Length 2067; | | | |
| Matches | 93; | Conservative | 76; | Mismatches | 144; |
| | | Indels | 140; | Gaps | 15; |
| Oy | 66 | LAQEEENVLDEFLKNEFLDNVRAQLSQDKER-----RPSQVITDPLTE----- | 112 | | |
| Db | 1655 | leqeenkvrlaqk--elsqrgqelldrrgekeefentrknhqraldsqasleaekg | 1711 | | |
| RESULT | 24 | | | | |
| ID | AAE02245 | AAE02245 standard; Protein: 875 AA. | | | |
| XX | | | | | |
| AC | AAE02245; | | | | |
| XX | | | | | |
| DT | 31-JUL-2001 | (first entry) | | | |
| XX | | | | | |
| DE | Domestic mite Bt11 allergen. | | | | |
| XX | | | | | |
| KW | Mite; immunogenic protein; Bt allergen; therapy; atopic dermatitis; immediate hypersensitivity; systemic anaphylaxis; allergic rhinitis; asthma; antiallergic; antiinflammatory; immunosuppressive. | | | | |
| XX | | | | | |
| OS | Blomia tropicalis. | | | | |
| XX | | | | | |
| PN | WO200130817-A1. | | | | |
| XX | | | | | |
| PD | 03-MAY-2001. | | | | |
| XX | | | | | |
| PF | 10-OCT-2000; | 2000WO-AU01227. | | | |
| XX | | | | | |
| PR | 26-OCT-1999; | 99SG-0005313. | | | |
| PR | 18-JUL-2000; | 2000AU-0008842. | | | |
| PR | 18-JUL-2000; | 2000AU-0008844. | | | |
| PR | 18-JUL-2000; | 2000AU-0008845. | | | |
| XX | | | | | |
| PA | (UYS1-) | UNIV SINGAPORE NAT. | | | |
| XX | | | | | |
| PI | Chua KY, | Cheong N, | Lee BW; | | |
| XX | | | | | |
| DR | WPI; | 2001-308609/32. | | | |
| DR | N-PSDB; | AA066237. | | | |
| XX | | | | | |
| PT | Novel immunogenic protein derived from house mite, Blomia tropicalis | | | | |
| PT | useful for treating and diagnosing conditions involving induction of immuneresponse to mite, such as allergic asthma, atopic dermatitis, rhinitis. | | | | |
| PS | Disclosure; Page 162-166; 230pp; English. | | | | |
| XX | | | | | |
| CC | The present invention relates to immunogenic proteins, referred to as Bt allergens, derived from domestic mite (Blomia tropicalis). The specific allergens of the invention includes Bt-1, Bt-5 and Bt-2. The | | | | |

| | | | |
|-------------------|--|----------|----------------|
| PR | 27-APR-2000; 200005-0560875. | Db | 634 yllesvrqrd |
| PR | 20-JUN-2000; 200005-0580875. | | 643 |
| PR | 19-JUL-2000; 200005-0620325. | RESULT | 30 |
| PR | 01-SEP-2000; 200005-054936. | AAB96332 | |
| PR | 15-SEP-2000; 200005-0633561. | ID | AAB96332 |
| PR | 20-OCT-2000; 200005-0693325. | AC | AAB96332; |
| PR | 30-NOV-2000; 200005-0728422. | XX | |
| PA | (HYSE-) HYSEQ INC. | XX | |
| XX | Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y; | XX | |
| PI | Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; | XX | |
| PI | Xue AJ, Yang Y, Weijhman T, Goodrich R; | XX | |
| XX | WPI: 2001-476283/51. | XX | |
| DR | N-FSSDB; AAK53255. | XX | |
| XX | Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy | XX | |
| PT | XX | XX | |
| PS | Claim 20; Page 430; 6221PP; English. | PS | |
| XX | The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AM78123-AM8002) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. | XX | |
| CC | Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication. | XX | |
| SQ | Sequence 690 AA; | SQ | |
| XX | Query Match 6.9%; Score 164.5; DB 22; Length 690; Best Local Similarity 23.3%; Pred. No. 9.1e-05; Matches 100; Conservative 64; Mismatches 129; Indels 137; Gaps 20; | XX | |
| QY | 64 FDLAQEEENVLDRBFL---KNELDNVRAQLSOKDEKEFRDSQVIIIDTLDLEERNATWV 119 | CC | |
| Db | 269 ydkvkserdalegevieirrkhealeashmiqukerselskevv-----tleg---tv 319 | CC | |
| QY | 120 SLQ---QALGKAEM---LCSTLUKKQMMYLEQQQDETPTQAAEE-----AGRURSKMK- 164 | CC | |
| Db | 320 llqkdkeylnrqmelsvraheedrlrlqgaleeskareemeykyvasrdhyktey 379 | CC | |
| QY | 165 -----TMEQIELLUQSOLQPEVEEMIRDKGVGQSAVEQLAQVYCVSLKKYENKEARKASG 219 | CC | |
| Db | 380 nkhdeledegirktnqneqdqinrasrem-----yernnnnirear-dn 421 | CC | |
| QY | 220 EVADKLK-----KDL-----FSSRSKLOQWYE----- 242 | CC | |
| Db | 422 avaekeeravmaekdalekhdqlddryrelqlsteskvtfingkskffeservqlqee 481 | CC | |
| QY | 243 ---LDQAKLKELEKSAQKQDLSQADKEIMSL---KKKLTM-----QETLNIPPVASET 287 | CC | |
| Db | 482 tarnltqsgceckykklevitkefyqlsassekkitelqaqpsenqardiyekle 541 | CC | |
| QY | 288 VDRULVLESFAPVENKLKRPSPFDDIDUNATEFDVTPFAPRSSSSORGYYEKICLESHS 347 | CC | |
| Db | 542 ldeimqk---aeinadedeervfysyganvp---ttkrrlkqsvharrvqleks 597 | CC | |
| QY | 348 PIQDVKPKCKGPRKESQISLGQSCAGEPDEELVGAFFIVR---NAILCQ-KOPKR 401 | CC | |
| Db | 598 li-----lkrsgstkspsnta-----frtslteamslngtqpyr 633 | CC | |
| 402 PRSESSCCR 411 | | CC | |
| Db | 634 yllesvrqrd 643 | Db | 634 yllesvrqrd |
| RESULT | 30 | RESULT | 30 |
| AAB96332 | | AAB96332 | |
| ID | AAB96332 | ID | AAB96332 |
| AC | AAB96332; | AC | AAB96332; |
| XX | | XX | |
| XX | DT 29-OCT-2001 (first entry) | XX | |
| XX | DE Putative P. abyssi ATPase involved in DNA repair #2. | XX | |
| XX | KW Hyperthermophilic archaeon; hyperthermophilic protein. | XX | |
| XX | OS Pyrococcus abyssi. | XX | |
| XX | PN FR2792651-A1. | XX | |
| XX | PD 27-OCT-2000. | XX | |
| XX | PF 21-APR-1999; 99FR-0005034. | XX | |
| PR | 21-APR-1999; 99FR-0005034. | PR | |
| XX | (CNRS) CNRS CENT NAT RECH SCI. | XX | |
| PA | (CNRS) CNRS CENT NAT RECH SCI. | PA | |
| PA | (IFRE-) IFREMER INST FR RECH EXPL MER. | PA | |
| XX | XX | XX | |
| XX | Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O; | XX | |
| PI | PI Querellou J, Weissenbach J, Saurin W, Heilig R; | PI | |
| XX | DR WPI: 2001-126236/14. | XX | |
| XX | PT New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry | PT | |
| XX | XX | XX | |
| PS | Claim 7; Pages 1003-1006; 1657PP; French. | PS | |
| XX | The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAK12227) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. | XX | |
| CC | CC Note: this patent is in the same patent family as WO2000505062, which contains additional sequences as shown in AAB99132-AAB99143, AAH15903-AAH15920 and AAG66436. | CC | |
| SQ | Sequence 880 AA; | SQ | |
| XX | Query Match 6.9%; Score 164.5; DB 22; Length 880; Best Local Similarity 21.9%; Pred. No. 0.00013; Matches 61; Conservative 65; Mismatches 122; Indels 31; Gaps 7; | XX | |
| QY | 65 DLAQEEENVLDRBFLKNELDNVRAQLSOKDEKEFRDSQVIIIDTLDLEERNATWV 124 | QY | |
| Db | 226 elekvenvkeleskgkisekiqvekkgrgkgleekivqierskeekakiseei 285 | Db | |
| QY | 125 LGKRAEMLCLSTLUKKQMMYLEQQQDETPTQAAEE-----KKEENLKEARKL-----RK 227 | QY | |
| Db | 286 vkdplqdekekeyrkgrfrdeyeeskirklekkewesekaleevikegekkerae 345 | Db | |
| QY | 182 EMIRDMGVQGQSAVEQLAQVYCVSLKKYENKEARKASG-----ASGEVADL----- 405 | QY | |
| Db | 346 eirekselekelelkpyveledaqvqkqerlkarlkqjgspgevikieslekert 405 | Db | |
| QY | 228 DLFSSRSKLOQWYESELDQAKLEKSAQKDLQSA-----DKSIMSLKKLMLQETNL 280 | QY | |
| Db | 406 eieeakiteittrigqmegeknemkaleelrkakgkpcvgrelteehkkelmyrtlei 465 | Db | |

| | | | |
|-----------------------|-------------|---|-----|
| Db | 321 | hievkesi-takecrailgttevralrileekesfinktkqlqdteekgtlageir | 379 |
| Qy | 79 | -----LKNELDNVVAQSLQDKDKERDQSVIDTDTLTERAVWSTQ | 123 |
| Db | 380 | dmkdmaleverkinvlqkkenlqeqrakdqgqtnlarkvslqdsnttdatallee | 439 |
| Qy | 124 | ALGKEMCSTLKKQMKYLIQEQEAGLRSKTMQIQLLQSREVEE | 183 |
| Db | 440 | alsekerilerlk----eqreindrleefsrkendikevnalqetekess | 493 |
| DT | 13-FEB-2002 | (first entry) | |
| XX | DE | Novel human diagnostic protein #5131. | |
| XX | XX | Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. | |
| XX | OS | Homo sapiens. | |
| XX | DE | W0200175067-A2. | |
| XX | XX | 11-OCT-2001. | |
| PF | XX | 30-MAR-2001; 2001WO-US08631. | |
| PR | XX | 31-MAR-2000; 2000US-0540217. | |
| PR | XX | 23-AUG-2000; 2000US-0649167. | |
| PA | PA | (HYSE-) HYSEQ INC. | |
| PI | XX | Drmnac RT, Liu C, Tang YR; | |
| XX | XX | WPI; 2001-639362/73. | |
| DR | XX | N-PSDB; AAS63327. | |
| XX | PT | New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification or mutations responsive for genetic disorders or other traits and to assess biodiversity - | |
| PT | XX | Claim 20; SEQ ID No 35499; 103pp; English. | |
| PS | XX | The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polyucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic amino acid sequences of the invention. | |
| CC | CC | Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences . | |
| SQ | Sequence | 808 AA; | |
| Query Match | 6.9% | Score 164; DB 22; Length 808; | |
| Best Local Similarity | 20.5% | Pred. No. 0.00012; | |
| Matches | 76; | Conservative 74; Mismatches 153; Indels 68; Gaps 10; | |
| Qy | 30 | HLQCLQSFFETAPSRTFCQCRIOG-----KRTIINKLFFDLAQ-EEENVLDREF- 18 | |

| | | | |
|---|----|--------|--|
| XX | FT | Region | /note= "cell-associated region" |
| PA | FT | | 407..441 |
| (YIRO) ROCKEFELLER UNIV. | | | |
| XX | FT | | /label= anchor |
| PI | FT | | /note= "preferred anchor region for use in novel |
| Fischetti V; | FT | | fusion proteins; includes a 3 amino acid |
| XX | FT | | spacer between the consensus anchor motif |
| DR | FT | | and the hydrophobic segment" |
| XX | FT | Region | 298..370 |
| PT | FT | | /label= carbohydrate_segment |
| for providing protection against streptococcal infection | FT | | 371..416 |
| XX | FT | | /label= peptidoglycan_segment |
| PS | FT | | /note= "consensus LPSTGE motif common to anchor |
| Disclosure; Fig 1; 22pp; English. | FT | | regions of gram-positive bacteria" |
| XX | FT | Region | 407..412 |
| CC | FT | | /label= hydrophobic_segment |
| Group A Streptococci; coiled coil surface antigen; anchor region; | FT | | 436..441 |
| gram positive bacterium; M protein; fusion protein; immunogen. | FT | | /label= "tail_segment" |
| XX | FT | Region | /note= "highly charged" |
| SQ | FT | | |
| Sequence 441 AA: | | | |
| Query Match 6.9%; Score 163.5; DB 10; Length 441; | | | |
| Best Local Similarity 22.3%; Pred. No. 5.9e-05; | | | |
| Matches 81; Conservative 70; Mismatches 124; Indels 89; Gaps 14; | | | |
| QY 55 KRNINNKFDLQAQEENVLDFEFLKNEFLNVRQLSQDKD-EKRDQSVIITLDTLE 112 | | | |
| 124 kktldetvkdkiakeqsketigtigtktld-----tvdkdkaekedesketigtigtktld 178 | | | |
| DB 113 ERNATVVLQALGKAEMLCSLKKQMKYLEQQDET-----KQAEEARGLRSKMK 164 | | | |
| 179 etvkdkiakeq--esketigtigtkil-----tvdkdkaekeskqkdigalkq-- 225 | | | |
| QY 165 TMQIELLILQSLQPEVER----MIRDNGVGSOSAVEOLAVRCVSLKEYENIKEARKASS 219 | | | |
| DB 226 -----elakdkgnvseasrkgrroldasreakqvekvdlanltaedkvkeekqisd 280 | | | |
| QY 220 EVADKLKDLSRSRSLQTVISLDQAKLELSAQKQDLSADKEIMSLKKITMLOETLN 279 | | | |
| 281 asrgqirridasr-----eak---kqvekaleeanskiaalekinkleees-- 324 | | | |
| DB 280 LPPVASETVDRLVLESAPVENVLKLRRPSFRDDIDNA-----TFDVDTTPARP 329 | | | |
| QY 325 -----kktkekakelqgkkaeakalkeqlqgqaaelaklragkadsqtpdakp 375 | | | |
| DB 330 SSSOHGYYEKLCLEKSHSPIDQPKTCKGPRKRESQLSLLGGSOSAGERDEELVGAFFIFV 389 | | | |
| DB 376 gn-----kvvpqkqgapqagtkpkqnkapmketkrql--pstget----anpift 419 | | | |
| QY 390 RNAAI 393 | | | |
| DB 420 aaall 423 | | | |
| RESULT 35 | | | |
| AAAR41780 | | | |
| ID AAAR41780 standard; protein: 441 AA. | | | |
| AC | | | |
| AAAR41780; | | | |
| XX | | | |
| DT 25-MAR-1994 (first entry) | | | |
| XX | | | |
| DE Streptococcus pyogenes M6 protein. | | | |
| XX | | | |
| KW Group A Streptococci; coiled coil surface antigen; anchor region; | | | |
| KW gram positive bacterium; M protein; fusion protein; immunogen. | | | |
| XX | | | |
| OS Streptococcus pyogenes. | | | |
| XX | | | |
| Key Region 1..362 | | | |
| FT /label= "extracellular_region" | | | |
| FT /note= "coiled structure" | | | |
| FT Region 298..441 | | | |

| | |
|-----------------------|--|
| PP | 26-DEC-2000; 2000WO-US34263. |
| XX | |
| PR | 21-JAN-2000; 2000US-0488725. |
| PR | 25-APR-2000; 2000US-0553117. |
| PR | 09-JUL-2000; 2000US-059042. |
| PR | 19-JUL-2000; 2000US-0620312. |
| PR | 03-AUG-2000; 2000US-065450. |
| PR | 14-SEP-2000; 2000US-0662191. |
| PR | 19-OCT-2000; 2000US-0693036. |
| PR | 29-NOV-2000; 2000US-0727344. |
| PA | (HVSSE-) HYSEQ INC. |
| XX | |
| PI | Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; |
| PI | Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J; |
| PI | Zhao QA, Zhou P, Goodrich R, Dumanac RT; |
| XX | |
| WPI; | 2001-442253/47. |
| DR | N-PSDB; AAI159172. |
| XX | |
| PT | Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - |
| XX | |
| PS | Example 4; SEQ ID NO 3161; 1007pp; English. |
| XX | |
| CC | The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (RAM8642-RAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. |
| CC | Note: The sequence data for this patent did not form part of the printed specification. |
| CC | Sequence 1213 AA; |
| SQ | |
| Query Match | 6.9%; Score 163.5; DB 22; Length 1213; |
| Best Local Similarity | 23.5%; Pred. No. 0.0024; |
| Matches | 109; Conservative 70; Mismatches 170; Indels 115; Gaps 20; |
| QY | 39 ETAPSRCTCPOCRIQVKRPIINKL-FFDLQAQEEENVLREFKLNEQDNRAQLSOKDK 95 |
| Db | 173 ekchhrtvylelenkhtydmksadfttulege---rerikalleqekaygarkek 227 |
| QY | 96 E-+KRDSQWVLTDRDTELEERNATVWSLQOALGKAEMLCSTIKQKYLEQQDERTKQAQ 153 |
| Db | 228 enakr---lnkrdelvklksfaml--vderqmhiqeqlgqs--qkvqdtqklr 276 |
| QY | 154 EEAQRLS-KMKTQMOIETLSQL-----PEVEMIRDMDVGOSAVEQALAVCV 202 |
| Db | 277 eeeeklkaatskskdrqkliklevdfehkasrfqsehennmakangqeshnqrlklv 336 |
| QY | 203 SLKKEYENLKEARK-----ASGEV-----ADKLKDIFSS---- 232 |
| Db | 337 gltqrieeleetnknlqkaeeelgeldrikakgecognsimaevenlrkvlemegdee 396 |
| QY | 233 -----RSKQTVYBFLDQAKLELMSAQDQKQDLSADK-EIMSLLKKLMLQENLNL 280 |
| Db | 397 itktesqcrelrikkiqeeehhskeirleveklikrmseleleafsksksectqhlhl 456 |
| QY | 281 PPVASETVDI-----VLESPAP---VENVNLKLRPSRFDDIDLNATFDPVNPAPRSS 332 |
| Db | 457 ekekHSEKTLKDLNLelevkrskeleceesre:lekaelsklkdkltkksftvmlvderin-- 514 |
| XX | |
| Query Match | 6.9%; Score 163.5; DB 22; Length 1639; |
| Best Local Similarity | 21.7%; Pred. No. 0.00036; |
| Matches | 117; Conservative 72; Mismatches 220; Indels 129; Gaps 21 |
| QY | 7 CTICSDFFDHSRDVAIHCQHTFLHQCLTOSFETAPSRTCPQCIQVKRMITNLFFDL 66 |
| Db | 1047 cidepcdcnlvqdadhlhraklfnsqtdieartpvtnddefe--akikavqekvavl 1103 |
| QY | 67 AQEEN-----VLDREFKLNEQDNRAQLSOKDKEKRSQVDTLDRLEARN 115 |
| Db | 1104 agqrdrnsdggtqyaivid--lhkhdsvrehsadqfqaadgeldar----qn 1156 |

| | |
|-----------------------|--|
| QY | 116 ATVV-----SIQQAIG----KAEMUCSTLKKOMKYLEQQQDETQKAQEEAGRRLS 161 |
| Db | 1157 ytdqiteakkelqqaclndegaqalarakeksvef gqseqisdisrealad 1215 |
| Qy | 162 KMKMEOIL-----LLQSQIPEVEMIRGMGGGSAVEOLAVCV 202 |
| Db | 1216 kieseaqknakdakdavakbqklaikdilqkigtersevqleishvqk---- 1269 |
| Qy | 203 SLKKEVENKEARRASGEADKLKDLFSSRSKLOTVSBDQAKLEMSAQDQASDK 262 |
| Db | 1270 slgtrvqtkelarckaneyd-----haltlindv-hrtqpeidiqkqkavaane 1321 |
| Qy | 263 EIMSLKKKJMLQETLNLPVASETVDRLVLESPAPVENLKLRRPSFRDDIDL---NA 318 |
| Db | 1322 radeilkqtelnsngelfadfeteqel-----tealikraeqqqiedielearka 1374 |
| Qy | 319 TFDVDTPPARPSSS---OHGYYKLC-----LESHSPTOPVPRKICKGPRKESQ 365 |
| Db | 1375 ahdkatkavveqgdhtlekaanntyeklagfqsdvgrssesaekalqtvp----niekeiq 1429 |
| Qy | 365 LSTGQSCGEPEPDVLFVGAPEFIVRNAIGQKQP-----KPRSESS 407 |
| Db | 1430 --naeslisqaaealda---nknaneaknakeaqkyaeqaskdakelirkanetk 1482 |
| Qy | 408 CSDKVVRGCFDGLGGRTRKTIQPTDVTMPLPVLVPKTKWQRVRYKTVPSLFFQAKLDT 465 |
| Db | 1483 vaarnlreadqinhrvkite-mdifkiesstkdnnlvdakr----kvqgakadt 1534 |
| RESULT 39 | |
| ID | AY07031 standard; Protein; 1752 AA. |
| XX | |
| AC | |
| XX | |
| DT | 02-JUL-1999 (first entry) |
| DE | Breast cancer associated antigen precursor sequence. |
| XX | |
| KW | Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer. |
| KW | |
| OS | Homo sapiens. |
| XX | |
| PN | W09904265-A2. |
| PD | 28-JAN-1999. |
| XX | |
| PF | 15-JUL-1998; 98W0-US14679. |
| PR | 22-JUN-1998; 98US-0102322. |
| PR | 17-JUL-1997; 97US-086164. |
| PR | 10-OCT-1997; 97US-0001599. |
| PR | 10-OCT-1997; 97US-0001765. |
| PR | 10-OCT-1997; 97US-0948705. |
| PR | 11-OCT-1997; 97GB-0021697. |
| PA | (LUDW-) LUDWIG INST CANCER RBS. |
| XX | |
| PI | Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ; |
| PI | Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E; |
| PI | Tureci O; |
| DR | WPI; 1999-132448/11. |
| XX | |
| PS | New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers |
| PS | Disclosure: Page 409-413; 787pp; English. |
| Query Match | |
| Best Local Similarity | 6.9% |
| Matches | 96 |
| Conservative | 96 |
| Mismatches | 156 |
| Indels | 125 |
| Gaps | 22 |
| Qy | 15 DHSRVAIAHCGHTFHQLQIOTSEFAPSPRTCPQCRIOVGRTTINNLFPLAQEBENVL 74 |
| Db | 68 eyenekavrnhyneemsnrnkvet-----einittti----keisngkd-- 111 |
| Qy | 75 DREFELNEDLVRAQISQKDEKRSQVQID---TLDTLERNAVTISIQLQALGKEMLC 132 |
| Db | 112 dsknlqnd----rsrenrdkidevlrnlndislnqdrteqrarraealaggkacoseimq 167 |
| Qy | 133 ST-LKKMKYLEQQDET---KQEEAGR-LKKMKTBEQIILQ-----S 175 |
| Db | 168 kkqhtielkqymqgsednarhkslesaktiqdknkeerkafqeeakrveyen 227 |
| Qy | 176 QLPEV----EEMI-----RDMGVGQSAVEQAVY---CVSLKKEYENKEARRASG 219 |
| Db | 228 elskvrrnnydeelisknqfsteinntktthqntkeedtsqyraqidaltrernsls 287 |
| Qy | 220 EVADKURKDKLFSRSRSLQTVSSELQAK-----LELUSA-----Q 254 |
| Db | 288 eeikrktntlqttenlrveediqgkatsgevsarkqlevelrqvtqmrteesvryk 347 |
| Qy | 255 KDLQSADEKIMSLKKITMLOETLNLPVASETVDRLVLESPAPVENLKLRRPSRDI 314 |
| Db | 348 qslldaaaktiqdknkeierlkqid----ketndrkcle----denarigrvay---- 393 |
| Qy | 315 DLNATFVDTTPPARPSSSOHGY----YKLCLKSHSPIDQYKPKICKGPRKESOLS 367 |
| Db | 394 dlqkassatetinkikvqsgelt:ridervsdrvskp-qiit--fenslkslq 450 |
| Qy | 368 LGGQSCAGEPDEELVGAPEFIVRNAIGQKOPKRSESSCSKDVVTGFDGL 420 |
| Db | 451 -----kqkveeel-----nrlkrasedskrkleelegm 482 |
| RESULT 40 | |
| AM41999 | |
| ID | AAM40999 standard; Protein; 1988 AA. |
| XX | |
| AC | AAM40999; |
| XX | |
| DT | 22-OCT-2001 (first entry) |
| XX | |
| DE | Human polypeptide SQ ID NO 5930. |
| XX | |
| OS | Homo sapiens. |

Search completed: September 4, 2002, 16:08:57
Job time: 8121 sec

